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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/977,034

DATE: 12/04/2001

TIME: 20:08:08

Input Set : N:\Crf3\RULE60\09977034.raw

Output Set: N:\CRF3\12042001\I977034.raw

1 <110> APPLICANT: Lo, Kin-Ming
2 Sun, Yaping
3 Gillies, Stephen D.
4 <120> TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
5 Fc Fusion Proteins
6 <130> FILE REFERENCE: LEX-009
7 <140> CURRENT APPLICATION NUMBER: 09/977,034
8 <141> CURRENT FILING DATE: 2001-10-11
9 <150> PRIOR APPLICATION NUMBER: US/09/575,503
10 <151> PRIOR FILING DATE: 2000-05-19
11 <150> PRIOR APPLICATION NUMBER: US 60/134,895
12 <151> PRIOR FILING DATE: 1999-05-19
13 <160> NUMBER OF SEQ ID NOS: 29
14 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 498
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(498)
23 <223> OTHER INFORMATION: Human IFN alpha DNA sequence
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26 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
27 1 5 10 15
28 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
29 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
30 20 25 30
31 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
32 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
33 35 40 45
34 cag aag gct caa gcc atc cct gtc ctc cat gag atg atc cag cag acc 192
35 Gln Lys Ala Gln Ala Ile Pro Val Leu His Glu Met Ile Gln Gln Thr
36 50 55 60
37 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
38 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
39 65 70 75 80
40 ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctg 288
41 Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
42 85 90 95
43 gaa gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg 336
44 Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
45 100 105 110
46 aat gtg gac tcc atc ctg gct gtg aag aaa tac ttc caa aga atc act 384
47 Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
48 115 120 125

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49      ctt tat ctg aca gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc      432
50      Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
51          130                      135                      140
52      aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa      480
53      Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu
54      145                      150                      155                      160
55      aga tta agg aag aag gat                                          498
56      Arg Leu Arg Lys Lys Asp
57          165
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 166
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
63 <400> SEQUENCE: 2
64      Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
65          1                      5                      10                      15
66      Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
67          20                      25                      30
68      Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
69          35                      40                      45
70      Gln Lys Ala Gln Ala Ile Pro Val Leu His Glu Met Ile Gln Gln Thr
71          50                      55                      60
72      Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
73          65                      70                      75                      80
74      Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
75          85                      90                      95
76      Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
77          100                     105                     110
78      Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
79          115                     120                     125
80      Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
81          130                     135                     140
82      Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu
83          145                     150                     155                     160
84      Arg Leu Arg Lys Lys Asp
85          165
87 <210> SEQ ID NO: 3
88 <211> LENGTH: 696
89 <212> TYPE: DNA
90 <213> ORGANISM: Homo sapiens
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)..(696)
94 <223> OTHER INFORMATION: Human Fc DNA sequence
95 <400> SEQUENCE: 3
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97      Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
98          1                      5                      10                      15
99      cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc      96

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100   Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
101           20                      25                      30
102   aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg   144
103   Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
104           35                      40                      45
105   gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg   192
106   Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
107           50                      55                      60
108   gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag   240
109   Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
110           65                      70                      75                      80
111   tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag   288
112   Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
113           85                      90                      95
114   gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc   336
115   Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
116           100                     105                     110
117   ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc   384
118   Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
119           115                     120                     125
120   cga gaa cca cag gtg tac acc ctg ccc cca tca cgg gag gag atg acc   432
121   Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
122           130                     135                     140
123   aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc   480
124   Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
125           145                     150                     155                     160
126   gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac   528
127   Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
128           165                     170                     175
129   aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat   576
130   Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
131           180                     185                     190
132   agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc   624
133   Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
134           195                     200                     205
135   tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag   672
136   Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
137           210                     215                     220
138   agc ctc tcc ctg tcc ccg ggt aaa                               696
139   Ser Leu Ser Leu Ser Pro Gly Lys
140           225                     230
142 <210> SEQ ID NO: 4
143 <211> LENGTH: 232
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
146 <400> SEQUENCE: 4
147   Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
148       1                      5                      10                      15
149   Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

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150          20          25          30
151  Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
152          35          40          45
153  Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
154          50          55          60
155  Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
156          65          70          75          80
157  Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
158          85          90          95
159  Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
160          100          105          110
161  Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
162          115          120          125
163  Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
164          130          135          140
165  Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
166          145          150          155          160
167  Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
168          165          170          175
169  Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
170          180          185          190
171  Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
172          195          200          205
173  Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
174          210          215          220
175  Ser Leu Ser Leu Ser Pro Gly Lys
176          225          230
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 27
180 <212> TYPE: DNA
181 <213> ORGANISM: Homo sapiens
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Forward PCR primer
184 <400> SEQUENCE: 5
185      cccgggtaaa tgtgatctgc ctcagac                                27
187 <210> SEQ ID NO: 6
188 <211> LENGTH: 26
189 <212> TYPE: DNA
190 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 6
192      ctcgagtcaa tccttcctcc ttaatc                                26
194 <210> SEQ ID NO: 7
195 <211> LENGTH: 162
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
198 <220> FEATURE:
199 <223> OTHER INFORMATION: IFN alpha consensus sequence wherein, Xaa at any
200      position besides positions 24,31,70 and 129
201      represents any amino acid.

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202 <223> OTHER INFORMATION: Xaa24 can be Ile or Leu, Xaa31 can be Lys or Gln,
203 Xaa70 can be Thr or Ser and Xaa 129 can be Leu or
204 Val.
205 <400> SEQUENCE: 7
W--> 206 Cys Asp Leu Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Leu Xaa
207 1 5 10 15
W--> 208 Xaa Xaa Xaa Xaa Met Xaa Xaa Xaa Ser Pro Xaa Xaa Cys Leu Xaa Xaa
209 20 25 30
W--> 210 Arg Xaa Asp Phe Xaa Xaa Pro Xaa Glu Xaa Xaa Xaa Xaa Xaa Gln Xaa
211 35 40 45
W--> 212 Xaa Xaa Xaa Gln Ala Xaa Xaa Val Leu Xaa Xaa Xaa Xaa Gln Gln Xaa
213 50 55 60
W--> 214 Xaa Xaa Leu Phe Xaa Xaa Xaa Xaa Xaa Ser Ala Xaa Trp Xaa Xaa Thr
215 65 70 75 80
W--> 216 Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gln Gln Leu Xaa Asp Leu
217 85 90 95
W--> 218 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
219 100 105 110
W--> 220 Xaa Val Xaa Xaa Xaa Leu Xaa Val Xaa Xaa Tyr Phe Xaa Xaa Ile Xaa
221 115 120 125
W--> 222 Xaa Tyr Leu Xaa Xaa Lys Xaa Xaa Ser Xaa Cys Ala Trp Glu Xaa Xaa
223 130 135 140
W--> 224 Xaa Xaa Xaa Xaa Met Arg Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu Xaa Xaa
225 145 150 155 160
226 Arg Leu
228 <210> SEQ ID NO: 8
229 <211> LENGTH: 166
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Human IFN alpha-1 protein
234 <400> SEQUENCE: 8
235 Cys Asp Leu Pro Glu Thr His Ser Leu Asp Asn Arg Arg Thr Leu Met
236 1 5 10 15
237 Leu Leu Ala Gln Met Ser Arg Ile Ser Pro Ser Ser Cys Leu Met Asp
238 20 25 30
239 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
240 35 40 45
241 Gln Lys Ala Pro Ala Ile Ser Val Leu His Glu Leu Ile Gln Gln Ile
242 50 55 60
243 Phe Asn Leu Phe Thr Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Asp
244 65 70 75 80
245 Leu Leu Asp Lys Phe Cys Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
246 85 90 95
247 Glu Ala Cys Val Met Gln Glu Glu Arg Val Gly Glu Thr Pro Leu Met
248 100 105 110
249 Asn Ala Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Arg Arg Ile Thr
250 115 120 125
251 Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val

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VERIFICATION SUMMARY

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L:206 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:206 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:208 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:210 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:210 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:216 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:216 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:218 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:218 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:220 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:220 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
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L:222 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:222 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
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